

SUPPLEMENTARY MATERIALS

The footprint of recent and strong demographic decline in the genomes of Mangalitza pigs

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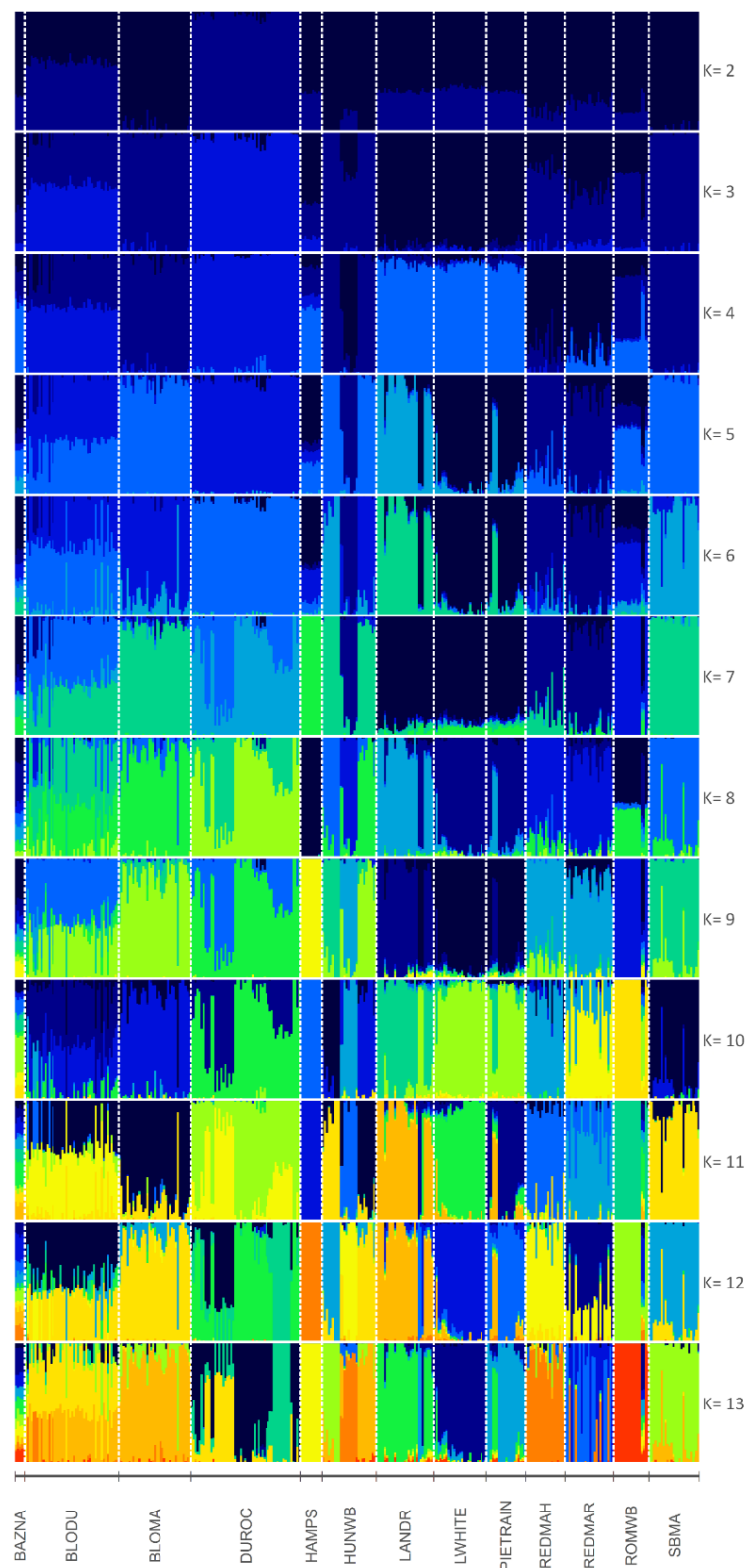
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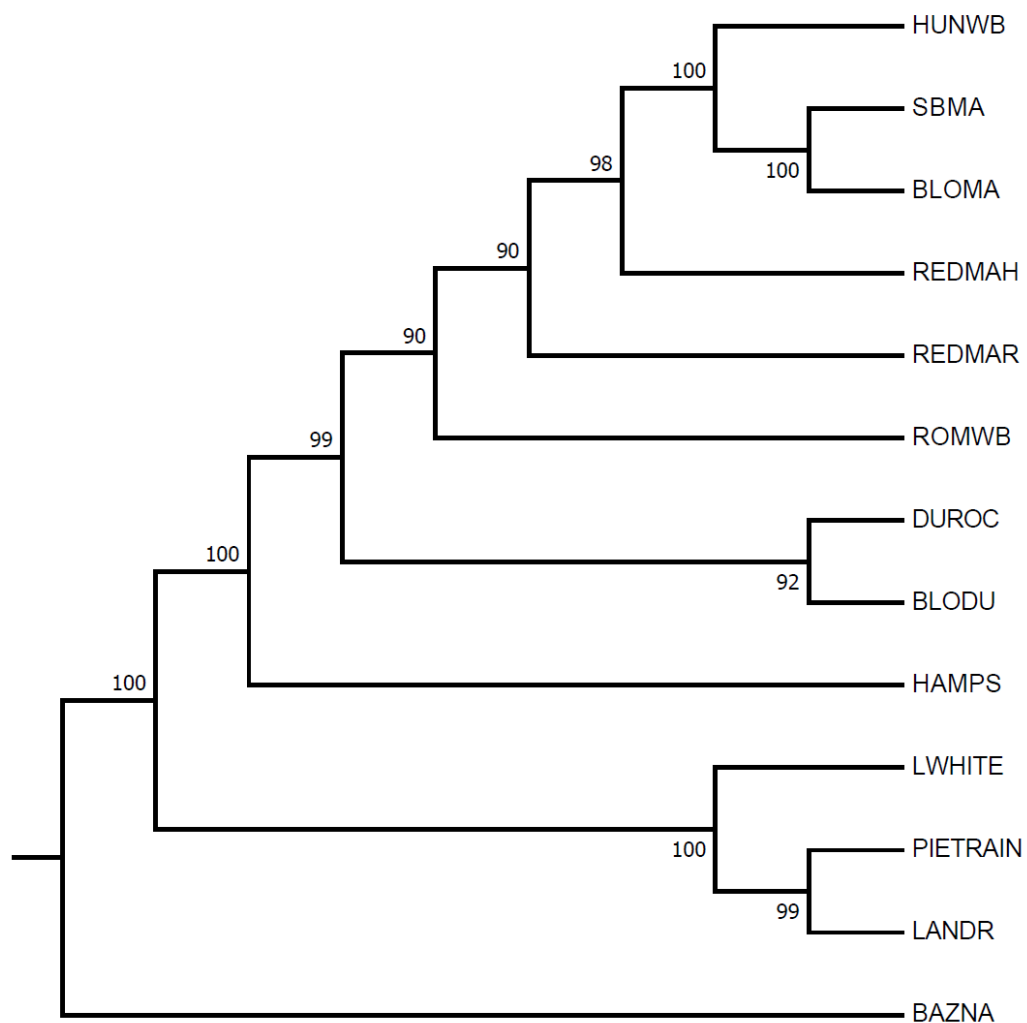
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Supplementary Figure S2. Admixture analysis of Mangalitza pigs and additional wild boar and pig populations for a range of K-values (K = 2 to 13). Each individual is represented by a single column divided into K colored segments, where K is the number of assumed clusters. Populations are separated by black lines. The following codes are used: DUROC = Duroc; BLODU = Blond Mangalitza x Duroc; HAMPS = Hampshire; BAZNA = Bazna; LANDR = Landrace; LWHITE = Large White; PIETRAIN = Pietrain; REDMAH = Red Mangalitza (Hungary); REDMAR = Red Mangalitza (Romania); BLOMA = Blond Mangalitza; SBMA = Swallow-belly Mangalitza; HUNWB = Wild boar (Hungary); ROMWB = Wild boar (Romania).

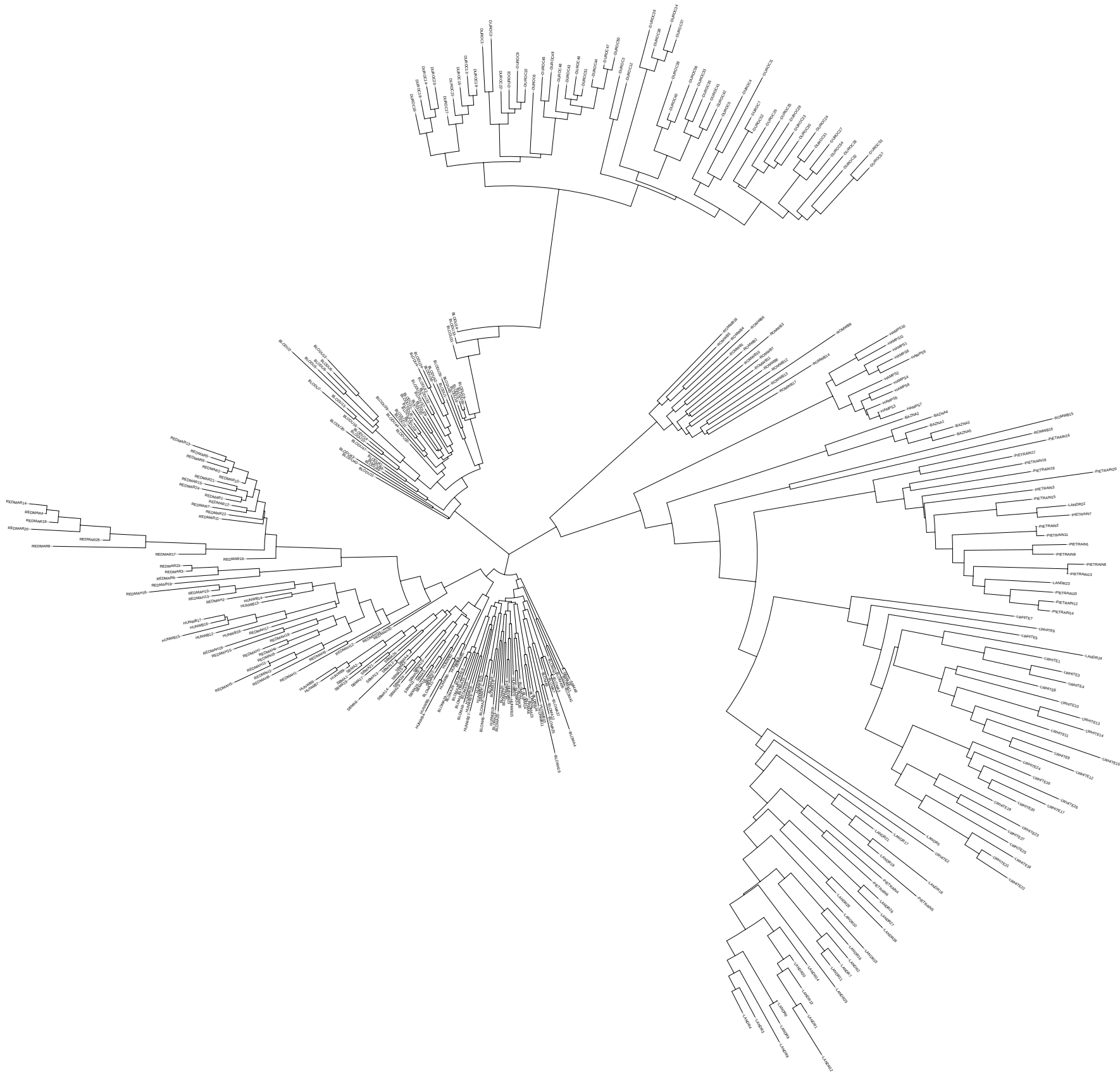


Supplementary Figure S3. Phylogenetic tree of Mangalitza pigs and additional wild boar and pig populations constructed with the TreeMix program. The following codes are used: DUROC = Duroc; BLODU = Blond Mangalitza x Duroc; HAMPS = Hampshire; BAZNA = Bazna; LANDR = Landrace; LWHITE = Large White; PIETRAIN = Pietrain; REDMAH = Red Mangalitza (Hungary); REDMAR = Red Mangalitza (Romania); BLOMA = Blond Mangalitza; SBMA = Swallow-belly Mangalitza; HUNWB = Wild boar (Hungary); ROMWB = Wild boar (Romania).

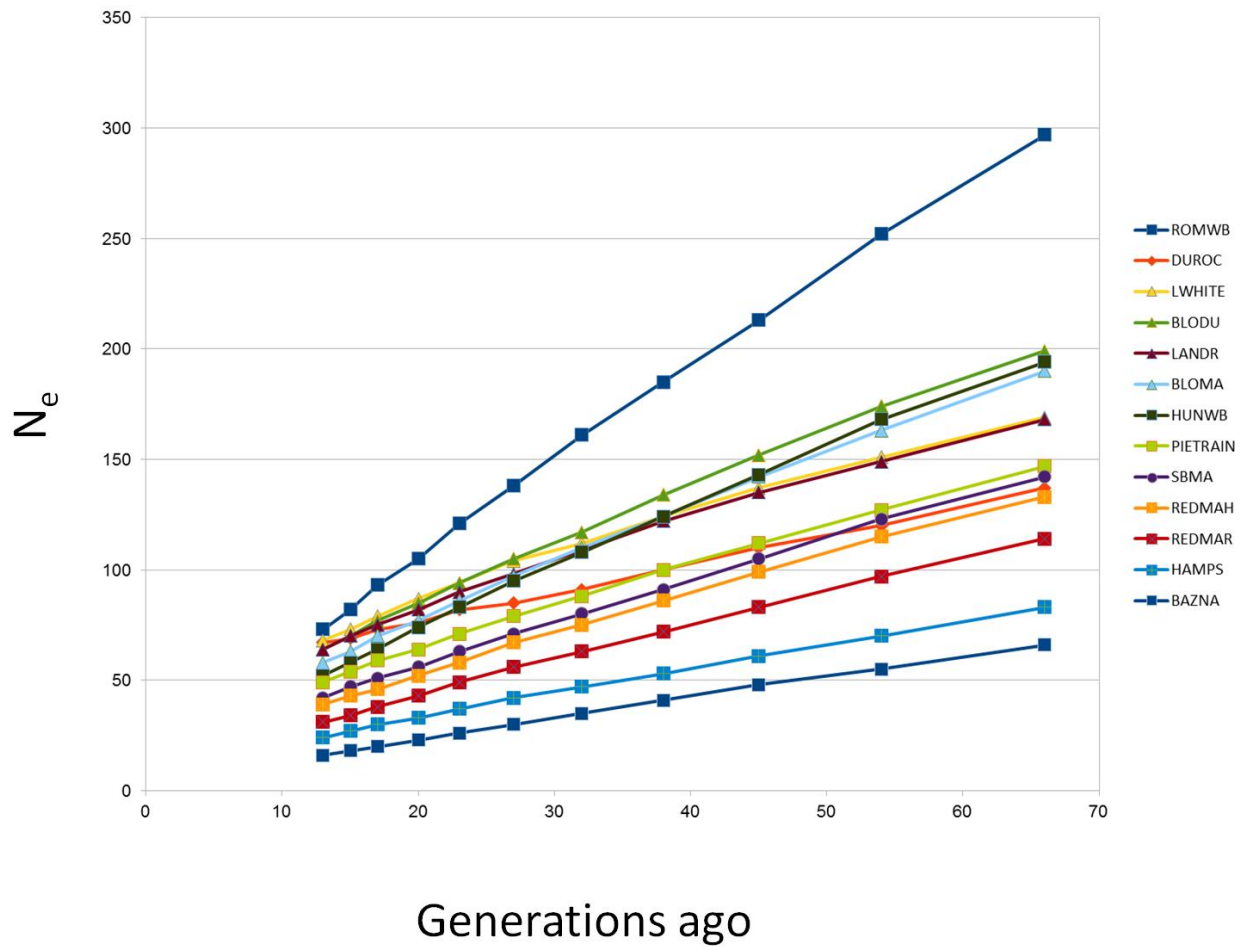
BAZNA	0	0.229	0.259	0.311	0.329	0.223	0.207	0.202	0.207	0.259	0.234	0.243	0.290
BLODU	0.229	0	0.118	0.096	0.238	0.111	0.179	0.182	0.183	0.147	0.16	0.175	0.158
BLOMA	0.259	0.118	0	0.282	0.274	0.031	0.212	0.223	0.218	0.132	0.17	0.168	0.085
DUROC	0.311	0.096	0.282	0	0.314	0.263	0.25	0.246	0.256	0.271	0.256	0.28	0.304
HAMPS	0.329	0.238	0.274	0.314	0	0.245	0.241	0.238	0.243	0.279	0.259	0.267	0.306
HUNWB	0.223	0.111	0.031	0.263	0.245	0	0.182	0.192	0.185	0.071	0.122	0.141	0.053
LANDR	0.207	0.179	0.212	0.25	0.241	0.182	0	0.125	0.108	0.201	0.18	0.196	0.236
LWHITE	0.202	0.182	0.223	0.246	0.238	0.192	0.125	0	0.115	0.204	0.175	0.198	0.246
PIETRAIN	0.207	0.183	0.218	0.256	0.243	0.185	0.108	0.115	0	0.206	0.181	0.196	0.24
REDMAH	0.259	0.147	0.132	0.271	0.279	0.071	0.201	0.204	0.206	0	0.115	0.185	0.166
REDMAR	0.234	0.16	0.17	0.256	0.259	0.122	0.18	0.175	0.181	0.115	0	0.186	0.201
ROMWB	0.243	0.175	0.168	0.28	0.267	0.141	0.196	0.198	0.196	0.185	0.186	0	0.195
SBMA	0.290	0.158	0.085	0.304	0.306	0.053	0.236	0.246	0.24	0.166	0.201	0.195	0
	BAZNA	BLODU	BLOMA	DUROC	HAMPS	HUNWB	LANDR	LWHITE	PIETRAIN	REDMAH	REDMAR	ROMWB	SBMA

Supplementary Figure S4. Graphical representation of pairwise coefficients of genetic differentiation (F_{ST}) values between Mangalitza pigs and additional wild boar and pig reference populations. The following codes are used: DUROC = Duroc; BLODU = Blond Mangalitza x Duroc; HAMPS = Hampshire; BAZNA = Bazna; LANDR = Landrace; LWHITE = Large White; PIETRAIN = Pietrain; REDMAH = Red Mangalitza (Hungary); REDMAR = Red Mangalitza (Romania); BLOMA = Blond Mangalitza; SBMA = Swallow-belly Mangalitza; HUNWB = Wild boar (Hungary); ROMWB = Wild boar (Romania).

Tree scale: 0.1



Supplementary Figure S5 (above). Neighbor-joining tree of Mangalitza pigs and additional wild boar and pig individuals. The following codes are used: DUROC = Duroc; BLODU = Blond Mangalitza x Duroc; HAMPS = Hampshire; BAZNA = Bazna; LANDR = Landrace; LWHITE = Large White; PIETRAIN = Pietrain; REDMAH = Red Mangalitza (Hungary); REDMAR = Red Mangalitza (Romania); BLOMA = Blond Mangalitza; SBMA = Swallow-belly Mangalitza; HUNWB = Wild boar (Hungary); ROMWB = Wild boar (Romania).



Supplementary Figure S6. Evolution of the effective population size (N_e) of Mangalitza pigs and additional wild boar and pig groups in the last 70 generations. The following codes are used: DUROC = Duroc; BLODU = Blond Mangalitza x Duroc; HAMPS = Hampshire; BAZNA = Bazna; LANDR = Landrace; LWHITE = Large White; PIETRAIN = Pietrain; REDMAH = Red Mangalitza (Hungary); REDMAR = Red Mangalitza (Romania); BLOMA = Blond Mangalitza; SBMA = Swallow-belly Mangalitza; HUNWB = Wild boar (Hungary); ROMWB = Wild boar (Romania).